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Db 601 GCAATATCAGCAGATGATTCACAAAGTGAATGTTGGAGCTAAATCAGTAATATGCA 660
QY 3714 TATCTGAAAGGAAAGTGCCTTCTGCTGGTGAATTCCTAGTCTAGTCTCTTCATT 3773
Db 661 TATCTGAAAGGAAAGTGCCTTCTGCTGGTGAATTCCTAGTCTAGTCTCTTCATT 720
QY 3774 GGAGTCTTTGAGAAAGTACTTTCAGACGACATTAATCAGGAGTGGCAAAAGAGTTGCA 3833
Db 721 GGAGTCTTTGAGAAAGTACTTTCAGACGACATTAATCAGGAGTGGCAAAAGAGTTGCA 780
QY 3834 ATTCTGACGAAAAAACTATCTGAGGAGACTTCAGCGCTTGTGTAATTCGACACAG 3893
Db 781 ATTCTGACGAAAAAACTATCTGAGGAGACTTCAGCGCTTGTGTAATTCGACACAG 840
QY 3894 ATTTAGATCTTTCAGACGACGATCAATTCCTCAAGAGCTGAAGAAAGATGACAGGT 3953
Db 841 GTTTAGATCTTTCAGACGACGATCAATTCCTCAAGAGCTGAAGAAAGATGACAGGT 900
QY 3954 TCTGGCATGCTTGGCCTGTGTATGAAGTTCACAAAGCGGTGGGACACAGCATGTGCG 4013
Db 901 TCTGGCATGCTTGGCCTGTGTATGAAGTTCACAAAGCGGTGGGACACAGCATGTGCG 960
QY 4014 ATAAAAAAGTGTGGGCTTCAAAATGCAATGAGAGACATCTTCAGCACAAGAGAGTG 4073
Db 961 ATAAAAAAGTGTGGGCTTCAAAATGCAATGAGAGACATCTTCAGCACAAGAGAGTG 1020
QY 4074 AAAGTGCATGATGATCTATCTGTGATGCTGCTCTGTTCAAGAAATTAATTAATGCTGAT 4133
Db 1021 AAAGTGCATGATGATCTATCTGTGATGCTGCTCTGTTCAAGAAATTAATTAATGCTGAT 1080
QY 4134 TATGATTTGTGATTCACACAAACCACTCTTCGAGAGACGACTCAGAAATATATGCG 4193
Db 1081 TATGATTTGTGATTCACACAAACCACTCTTCGAGAGACGACTCAGAAATATATGCG 1140
QY 4194 GAGTGTGACGCGCTTGGGAAACACTTGTGGAGCTTACCGAGGAGCGTGTGAT 4253
Db 1141 GAGTGTGACGCGCTTGGGAAACACTTGTGGAGCTTACCGAGGAGCGTGTGAT 1200
QY 4254 TTTATCTGCAAGAAAGATCTCAACTCTCTCAAGTGTAGTTACCAAGCAACCG 4313
Db 1201 TTTATCTGCAAGAAAGATCTCAACTCTCTCAAGTGTAGTTACCAAGCAACCG 1260
QY 4314 ATCGGCTTTTCATAAAAAGATCTATCTTCCGATGTGATTCGAATGGGGAAGATTG 4373
Db 1261 ATCGGCTTTTCATAAAAAGATCTATCTTCCGATGTGATTCGAATGGGGAAGATTG 1320
QY 4374 GAAGGTTATGCGGCTGCTGGCCTCTACGAGAGTGTACCAATGATGAGGAAAAAGTT 4433
Db 1321 GAAGGTTATGCGGCTGCTGGCCTCTACGAGAGTGTACCAATGATGAGGAAAAAGTT 1380
QY 4434 GTAATTGATTAATCTTCCGACCCATGATTAATGATGTAATTCGCGCAGACAATCCTG 4493
Db 1381 GTAATTGATTAATCTTCCGACCCATGATTAATGATGTAATTCGCGCAGACAATCCTG 1440
QY 4494 TCCACATTTGCTGCTGACATGATGAGGAGCTATATGGCTCTCTCAAGACATG 4553
Db 1441 TCCACATTTGCTGCTGACATGATGAGGAGCTATATGGCTCTCTCAAGACATG 1500
QY 4554 GAGGTTAGTGAAGGATGGAAGATTTATGCTTCAGACAGACCTCAGATGTATCA 4613
Db 1501 GAGGTTAGTGAAGGATGGAAGATTTATGCTTCAGACAGACCTCAGATGTATCA 1560
QY 4614 TATCTGCTGTATGTTGTTTCAGAGAGACCATAGATGTGATCATATCTCATGTTATCA 4673
Db 1561 TATCTGCTGTATGTTGTTTCAGAGAGACCATAGATGTGATCATATCTCATGTTATCA 1620
QY 4674 GATCTGTGACCACT-----TACCTCCCATGAAGTGTGCTGTATGATTAAGTGTATCC 4726
Db 1621 GATCTGTGACCACTTAAGTGTATGATTAAGTGTATGATTAAGTGTATCC 1680
QY 4727 AAAGCATCAGATCATGTTACCTTACGCTAATGAGAGAGAGTGAAGTGAAGTATGC 4786
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Db 1681 AAAGCATCAGATCATGTTACCTTACGCTAATGAGAGAGAGTGAAGTGAAGTATGC 1740
QY 4787 AATATGAGGATTAATAGAAAAAAGCTTTGTAGAGTTAAATTTAGTGGTATGATAGCG 4846
Db 1741 AATATGAGGATTAATAGAAAAAAGCTTTGTAGAGTTAAATTTAGTGGTATGATAGCG 1800
QY 4847 AGAATGTGTAACATTTGATATATATATATATATATATATATATATATATATATAT 4905
Db 1801 AGAATGTGTAACATTTGATATATATATATATATATATATATATATATATATATAT 1860
QY 4906 GCACGTGAATATATCGGACATCAAGAGAGAAATCCTTTGAGTGTGTTCA 4956
Db 1861 GCACGTGAATATATCGGACATCAAGAGAGAAATCCTTTGAGTGTGTTCA 1911
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## RESULT 9

AAZ30162 standard: cDNA: 2080 BP.

AC AAZ30162:

DT 26-JAN-2000 (first entry)

DE cDNA encoding a portion of the starch R1 phosphorylation protein.

KW Starch R1 phosphorylation protein; starch degradation;

KW plant starch biosynthesis; ~~starch~~

OS Glycine max.

FH Key Location/Qualifiers

FT CDS 3..1748

FT /\*tag= a

PN W09953072-A1.

PD 21-OCT-1999.

PE 08-APR-1999: 99WO-0507639.

PR 09-APR-1998: 98US-0081143.

PA (DUPLO) DU PONT DE NEMOURS &amp; CO E I.

PI Cressman RF, Allen SM;

DR WPI: 1999-620435/53.

DR P-PSDB: AAY43629.

PT New starch R1 phosphorylation protein homologues

PS Claim 2; Page 41-42; 54pp; English.

CC The present sequence encodes a starch R1 phosphorylation protein.

CC also describes a chimeric gene encoding all or a portion of the

CC starch R1 phosphorylation protein, in the sense or antisense

CC orientation, where expression of the chimeric gene results in

CC production of altered levels of starch R1 phosphorylation protein

CC in transformed plants or cells. The protein facilitates studies of

CC starch degradation in plants, and provides tools for the genetic

CC manipulation of starch biosynthesis in plants.

SQ Sequence 2080 BP; 623 A; 385 C; 467 G; 605 T; 0 other;

Query Match 20.4%; Score 1032.8; DB 20; Length 2080;

Best Local Similarity 74.9%; Pred. No. 6.5e-279;

Matches 1308; Conservative 0; Mismatches 432; Indels 6; Gaps 1;

QY 2869 AAATCATGACTTCACTCTGCTGCTGTAATAATCTGCACTCTCTGTGAGCAGATAATG 2928

Db 1 AAATTAATGTAATCTTCACTTGTGCTTCTTGAATAATCTGCACTTCTCATGGAAGCAATG 60

QY	2929	AAGATCTTGTATTGCTTGAAGGATGGAATCAACTCTTTCAATGTCGAATGCTGGAG	2988
DB	61	AAGATCTTATCTACTGTTTGAAGGATGGATGTTGCTTAAGCATGTGCAGATTAAAG	120
QY	2989	ACAACCATTTGGCTTTATTGTCAAAAAGCTGTACTTGACAGAAATCCGCTTGCACTTGCA	3048
DB	121	ATACTCATTTGGGCATTTGACGCAAAATCAGTCCCTGACAGAACCCGCTTGCACTAACAA	180
QY	3049	GCAAGCGAGAGTGTACCATCACTTATTGCAGCCATCTGCCGAATATCTAGATCAATCC	3108
DB	181	ACAAGGCTCATTTATTACCGAGAAATTTCTGCAACCATCGGACAGATATCTTGGATCACTCC	240
QY	3109	TTGGGGTGGACCAATGGGCTTTGAACATATTACTGAAGAAATTATACGTGCTGATCAG	3168
DB	241	TTGGCGTGACAAATGGCCCGTGGAAATATTACTGAAGAAATATCCGTGCTGATCTG	300
QY	3169	CAGCTTCATTATCCTCTCTCTTAAATAGACTGATCCCGTGTCTTGGAATACTGCAATC	3228
DB	301	CTGCTTCTTTGTCTACTCTCTTAATCGACTGATCCGTGCTCCGAAAGACAGCTCATC	360
QY	3229	TAGGAAGTTGGCAGATTATCAGTCCAGTGAAGCCGTTGGATATGTTGCTGTTGATG	3288
DB	361	TTGGAAGCTGGCAGGTTATTAGCCCAAGTTGAACCTGTTGATATGTTGAGGTCATAGATG	420
QY	3289	AGTTGCTTTCAGTTCAGATGAATCTACAAGAAGCCACGATCTTAGTAGCAACTCTG	3348
DB	421	AGTTGCTTGTCTGTCAAAACAATCATATGAGCGACTTACAATTTTGATAGCCAAGACTG	480
QY	3349	TTAAAGGAGAGAGAGAAATTCCTGATGCTGCTGTTGCCCTGATAACACCAGACATCCAG	3408
DB	481	TGAGAGAGAGAGAGAAATTCAGATGTGATGATGCTGCTGCTGACACCTGATATGCCG	540
QY	3409	ATGTTCTTTCACATGTTCTGTGAGCTAGAAATGGGAAGTTTGTCTTGTCTACATGCT	3468
DB	541	ATGTCCTATCCCATGTATCTGTAGCAGCAAGAAATAGCAAGTGTGTTTGTCTACATGCT	600
QY	3469	TTGATCCCAATATATTGGCTGACCTCCAGCAAGCAAGGAAGATTTTGCTCTTAAAGC	3528
DB	601	TTGATCCCAATATCTGCTGCTAACCTCCAGAAATTAAGGAAGCTTTTGGCGCTTAAAGC	660
QY	3529	CTACACCTTCAGACATTAATCTATAGTGAGGTGAATGAGTGTGAGCT----CCAAAGTT	3582
DB	661	CAACATCTGCTGATGTAGTTTATAGTGAGGTCAAGGAGGTGAGTTAATTGATGACAAAT	720
QY	3583	CAAGTAAGTGTGAGAACTGAACTTCAGCAACACTTAGATTGGTGAATAAGCAATTTG	3642
DB	721	CAACTCAACTCAAGAGATGTGCTTCTGTGTCACCCATATCTCTGCCCCGAAGAAGTTTA	780
QY	3643	GTGGTGTACCGCAATATCAGCAGATGAAATTCACAAGTGAATGTTGGAGCTAAATCAC	3702
DB	781	GTGGTAGATATGCTGTCTCATCTGAAGAATTCACGTGTGAATGTTGGAGCTAAATCTC	840
QY	3703	GTAATATTGCATATCTGAAAGGAAAAAGTGCTTCTCGGTGGGAATTCTCTACGTCAGTAG	3762
DB	841	GTAATATCTCTTATTAAAGGGAAGTAGCTTCTTGGAATTGGAATTCCTACCTCGGTTG	900
QY	3763	CTCTTCATTGTGAGTCTTTGAGAAAGTACTTTTCAGACGACATTAATCAGGGAGTGGCAA	3822
DB	901	CCATACCATTTTGAGTTTTCGAAACATGTTCTTTGTGATTAACCAACCAAGCAGTGGCTG	960
QY	3823	AAGAGTTGCAATTTTCAGCAAAAAAATCATCTGAAGGAGACTTCAGCGCTCTTGTGAAA	3882
DB	961	AGAGGTCATAATTTGAATAAAGAAAGACTTAATTGAGGAGACTTCAGTGTCTCAAGGAGA	1020
QY	3883	TTGGCACAAGGATTTAGATCTTTACAGCACCAAGTCAATTGGTCAAAAGAGCTGAAGGAAA	3942
DB	1021	TTGCTGAACACAGTTCTACAAATTTGAATGACCAATCCCAATTGGTAGAGAGTTGAACCTA	1080
QY	3943	AGATGACAGGTTCTGGCATGCTTGGCCTGCTGATGAAGGTCCAAAGCGGTGGAAACAAG	4002
DB	1081	AAATGAAGAGTTCTGGAATGCCCCGTGGCCGGGTGATGAAGGTGAACAACGATGGGACCAAG	1140
QY	4003	CATGATGGCCATAAAAAGGTGTGGGCTTCAAAATGCAATGAGAGCATACTTCAACA	4062

Db	1141	CTTGAGTAGCTATATAAAAAAGGTGGGGGCTTAAGTGAATGAAGACACTACTTCAGCA	1200
OY	4063	CAAGCAAAGGTGAAACTGCATCATGACTATCTGTGCATGGCTGTCTTTGTTCAAGAATAA	4122
Dd	1201	CAAGAAAAGTGAAACTCGAACCCAGCAATATCTTTCCATGGCAGTCCTTGTTCAGAAGTGA	1260
OY	4123	TAAATGCTGATTATGCATTTCTCATTTCCACACAACCACCATCTTCGGAGACGANTCAG	4182
Dd	1261	TAAATGCTGACTATGCTTTCTTCATCTCCACACAACCTAACCTGCCCTCGAGATTATCGG	1320
OY	4183	AAATATATGCCGAGGTGTCAGGGGCGCTTGGGAAACACTGTGTGAGCTTACCCATCAGC	4242
Dd	1321	AAATATATGCTGAGGTGTTAAAGGACTTGGAGAAACACTGGTTGAGCTTATCCAGCTC	1380
OY	4243	GTCCTTTGAGTTTATCTCGACAGAAAAAGGATCTCAACTCTCCTCAAGTGTAGTTACC	4302
Dd	1381	GTCCTTTGAGTTTATCTCGACAGAAAAAGGATTTGAACCTCTCCTCAGGCTTAGTTATC	1440
OY	4303	CAAGCAAACCGATCGGCTTTTCATAAAAAGATCTATCATCTTCCGATCTGATTCCAATG	4362
Dd	1441	CTAGCAAACCTGTGCGCCATTTATAGACGGTCAATATTTTCGATCTGATTCCAATG	1500
OY	4363	GGGAGAGATTGGAGGTTATGCCGCTGTGCGCTCTACACAGTGTACCAATGATTAAGG	4422
Dd	1501	GTTAGAGATCTAGAAGGATATGATGGTGCAGAGTCAATTAATGACAGTGTCCCAATGGGTGAC	1560
OY	4423	AGGAAAAAGTTGTAATTGATTACTCTTCCGACCCATTTGATTAACCTGATGTAACCTTCGCC	4482
Dd	1561	CCGAGAAGGTGTGCTGCTTGAATTACTTCTCACACAAACTGATCTTGATGGCAGTTTTCGCC	1620
OY	4483	AGACAATCCTGTGCCAACATTTGCTGCTGTGCAGACATGCTATGAGAGGCTATATGCTCTC	4542
Dd	1621	AGTCAATCTGTGCCAGCATTTGCCCGTGCAGGAAATGAATTGAAGAGTGTATGCGACTC	1680
OY	4543	CTCAAGACATCGAGGGTGTAGTGAGGAGTGAAGAGATTTATGCTGTCAGACAAGACTTC	4602
Dd	1681	CTCAGGACATTTGAAGGTGTCATCAAGGATGAAAAAGTCTATGTTGTCCAGACGACGCCAC	1740
OY	4603	AGATGT 4608	
Dd	1741	AAATGT 1746	
 RESULT 10 AAV44318 standard; cDNA to mRNA; 2307 BP.			
ID	AAV44318		
XX	AAV44318;		
DT	07-OCT-1998	(first entry)	
DE	Maize starch-associated protein cDNA.		
KW	Starch-associated protein; maize; starch grain; soluble;		
KM	transgenic plant; ss.		
OS	Zea mays.		
FH	Key	Location/Qualifiers	
FT	CDS	33..1946	
FT	/tag-	a	
FT	/product-	"starch-associated protein"	
FT	/note-	"no start codon given"	
PN	DE19653176-A1.		
PD	25-JUN-1998.		
Pf	19-DEC-1996;	96DE-1053176.	
PR	19-DEC-1996;	96DE-1053176.	